

• SID4

RESULT 2

S57294

LOCUS S57294 250 bp DNA MAM 28-JUN-1993

DEFINITION (D-loop region) [cattle, Mitochondrial, 250 nt].

ACCESSION S57294

VERSION S57294.1 GI:298691

KEYWORDS

cow.

SOURCE Mitochondrion Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 250)

AUTHORS Madsen, C.S., Ghivizzani, S.C. and Hauswirth, W.W.

TITLE Protein binding to a single termination-associated sequence in the
mitochondrial DNA D-loop region

JOURNAL Mol. Cell. Biol. 13 (4), 2162-2171 (1993)

MEDLINE 93204962

REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 127635] from the original journal article.
This sequence comes from Fig. 2.

COMMENT Sequence is identical to previously published sequence with
exception of an A-to-G transition at position 16079.

FEATURES Location/Qualifiers

:source 1..250
/organism="Bos taurus"
/organelle="mitochondrion"
/db_xref="taxon:9913"

BASE COUNT 92 a 46 c 34 g 78 t

ORIGIN

Query Match 100.0%; Score 46; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 attatatccccatgcataaaggcaagtacatgacctctatagcag 46

|||||||||||||||||||||||||||||||||||||||||

Db 73 ATTATATGCCCATGCATATAAGCAAGTACATGACCTCTATAGCAG 118

-continued

Ser Phe Asp Leu Leu Leu Ser Ser Lys Asn Gly Val Ala Ala Phe His
 65 70 75 80
 Ala Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Leu
 85 90 95
 Ala Cys Glu Glu Phe Lys Lys Ile Arg Ser Ala Thr Lys Leu Ala Ser
 100 105 110
 Arg Ala His Gln Ile Phe Glu Glu Phe Ile Cys Ser Glu Ala Pro Lys
 115 120 125
 Glu Val Asn Ile Asp His Glu Thr Arg Glu Leu Thr Arg Met Asn Leu
 130 135 140
 Gln Thr Ala Thr Ala Thr Cys Phe Asp Ala Ala Gln Gly Lys Thr Arg
 145 150 155 160
 Thr Leu Met Glu Lys Asp Ser Tyr Pro Arg Phe Leu Lys Ser Pro Ala
 165 170 175
 Tyr Arg Asp Leu Ala Ala Gln Ala Ser Ala Ala Ser Ala Thr Leu Ser
 180 185 190
 Ser Cys Ser Leu Asp Gln Pro Ser His Thr
 195 200 202

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 171..351
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTTAGAGCA ACTCAGGAAA TAGGTGCACA CAAGCAAACC ATGTGGTTAA AGCCTTTGGA	60
ACTGCTTCA CCAAAGCTGT AGCGTATTTC ACAAAATCAT CTGCAAAACC AGATTTCTAA	120
CACCTCCCTG CTGTGTATCT CATTCTGCT GATGTGTGGT GCTTCATAAG ATG CGG	176
ACG TTA AGC ATG CAG CAA CTA CAG TCA TTT GTT CTC AGA GGT CTG GAC	224
CAA AGA GAA ACA AGA AAA GCT GGA GTC ACA CTA CCA AAG GCC GAA GCT	272
GAG CAA CAG AGC TCT GGA GTC AGC TGC CTG GGT TCA GCA TGC AGC GCT	320
GCC GTG GAC GAT CTG TCT CTC TTG CAT ATA T GACTTACCAAG TTTTACTTTC	371
AGTCTCTCCA TTTCTAAATTA AATGAGATGC AGAAAATGCTG GTGCCCTGCT ATGATGTTTG	431
CAGTTATTAT TTCTAGGAAA AAAATATTTA TTGTTACTCA GTATCTGGTC TAGCTACTTG	491
GACAACCTGGA CTATCCCCCT CCTTTCAAGG GAGGGCAAAG CATTTCAGAA AAGAACTAAG	551
TGCTATTCTCT CGCTTCAGG AATGCTCTCC GTATGAAAAA GAATGTGGCT TCAGGGAGTA	611
GCATGTGTTG TAAAGGTGGA TGGGTCTAAC TTTCATGGACA GCTCTGACAT CCACTAGCTA	671
TGCCACCTGA TGCAAACAC TTGGGCTGTC TGCAGTTTCG TTTATCTTTC TGGAAATTGGT	731
AATAACAACC ACCTGGCAAG ATCACTGTTA TGAATACGGA GGATCAAAGT TGTGAAGTTA	791
TTTTGTAAAG TGAAATGTT TGAAAAATGG ATTTAACAG TGTCAAGCAG AAGTAGATT	851
TTGACATTAA TCAAGAGTTC AGCTAATGAA AACAACTATG GATAATAGTT ACATAGAACT	911
GTCTACTTTA CTCAGTACTT TAGCATATGC TATTATATT AATCTCTTA AAAAGTAGGA	971
AATTATACAA GCCATGTATT GATATTATTG TGGTGGTTGT CGTTCTCAAT TACACACTGA	1031